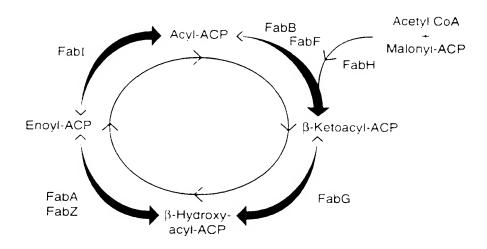
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Figure 1. The Cycle of Fatty Acid Elongation in Bacteria



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Figure 2. Synthesis of Deuterated Pyridine Nucleotides

## Synthesis of R-NADD

## Synthesis of S-NADD

Figure 3. Predicted (Observed) Product Structures and (M+H)+'s

(Based on E. coli Fab I)

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Figure 4. Mass Spectra of Components from Reaction 3

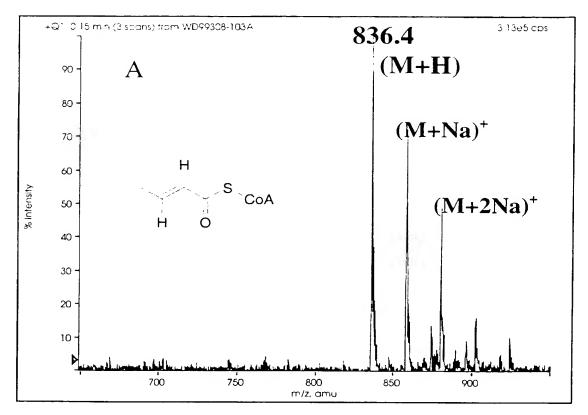


Figure 4 B

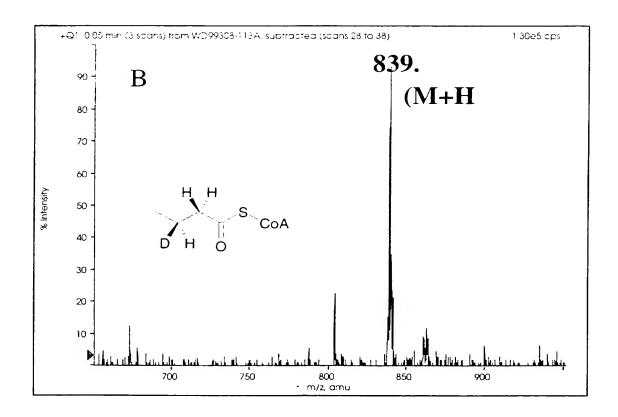
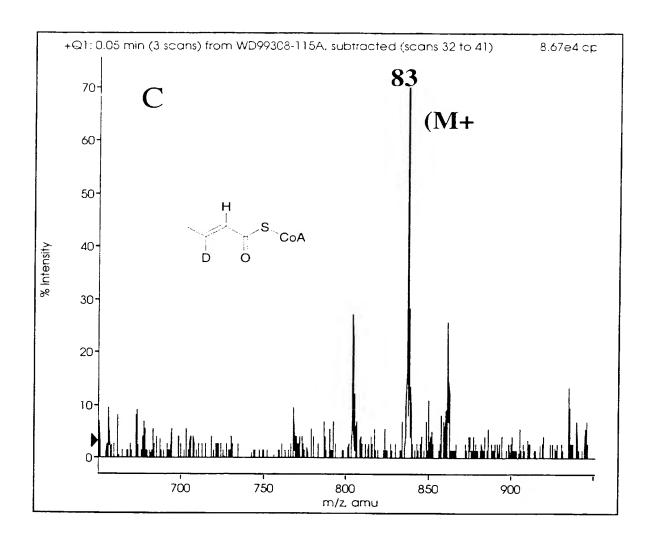


Figure 4 C



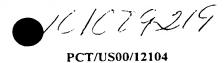
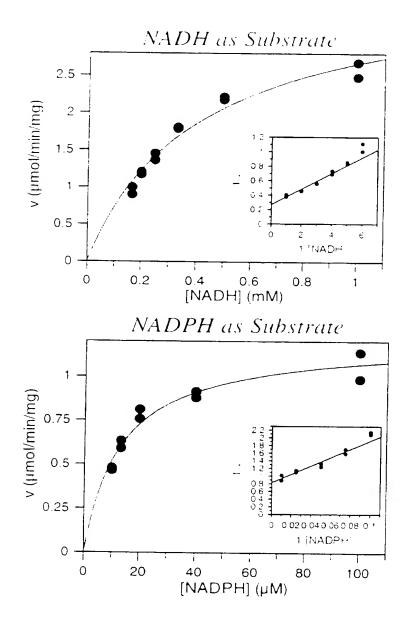


Figure 5. Stereochemical Course of S. aureus Fab I

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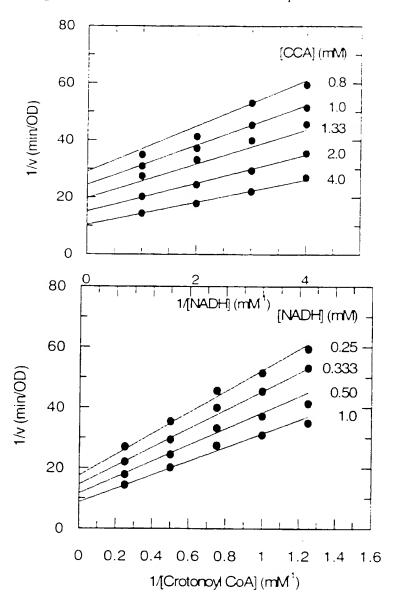
Figure 6. S. aureus Fab I Uses Both NADPH and NADH as Substrates



	NADH	NADPH
Vm(app) (µmol/min/mg)	3.75±0.23	1.21±0.06
Km(app) (mM)	0.41±0.06	0.013±0.002
Km(app) CCA (mM)	3.5±0.2	1.4±0.4

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Figure 7. S. aureus Fab I Exhibits a Sequential Mechanism

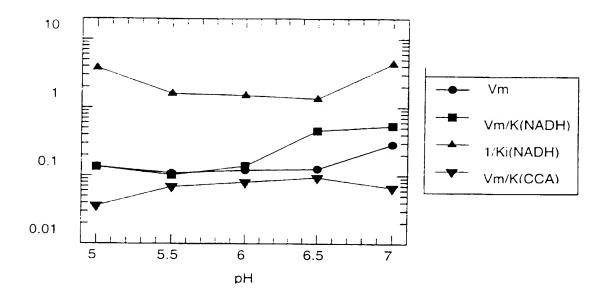


$$\begin{split} V_m &= 0.18 \pm 0.02 \\ K_a &= 0.52 \pm 0.12 \text{ mM} \\ K_b &= 3.3 \pm 0.6 \text{ mM} \\ K_{ia} &= 0.22 \pm 0.06 \text{ mM} \end{split}$$

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Figure 8. pH Profile of S. aureus Fab I



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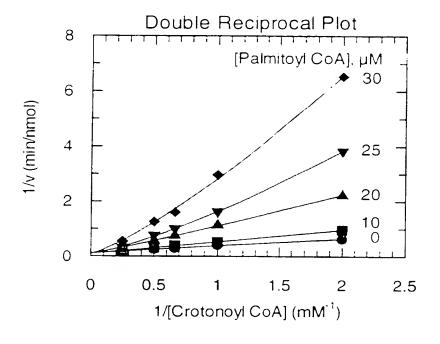
WO 00/70017

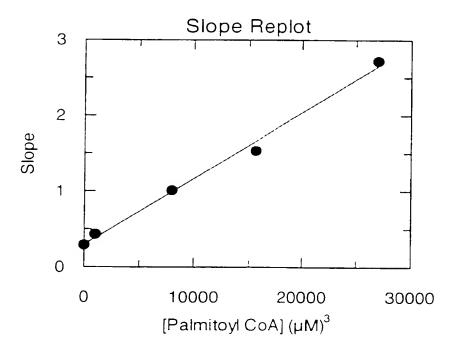
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Figure 8 A Table 1. Inhibition by Saturated Fatty Acyl CoA's

CoA Derivative		Mean $IC_{50}(\mu M)$ $(n=2)$		
A	cetyl	>>1000		
n-E	Butyryl	>>1000		
n-He	exanoyl	576		
n-O	ctanoyl	248		
$n$ - $D\epsilon$	rcanoyl	226		
La	uroyl	48.4		
$M_{N}$	ristoyl	23.1		
Pal.	mitovl	10.7		

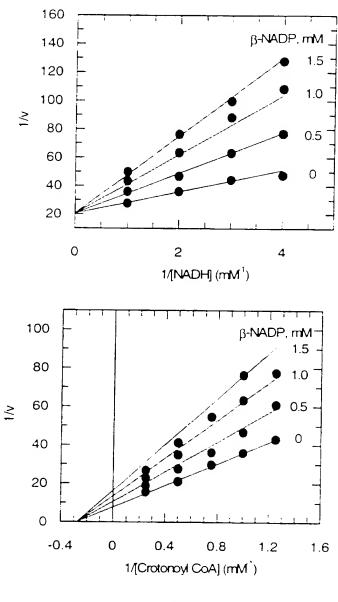
Figure 9. Inhibition by Palmitoyl CoA





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Figure 10. Inhibition by  $\beta$ -NADP<sub>+</sub>



 $Ki = 0.58 \pm 0.03 \text{ mM}$ 

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Figure 11. Kinetic Model for Inhibition by β-NAPD+

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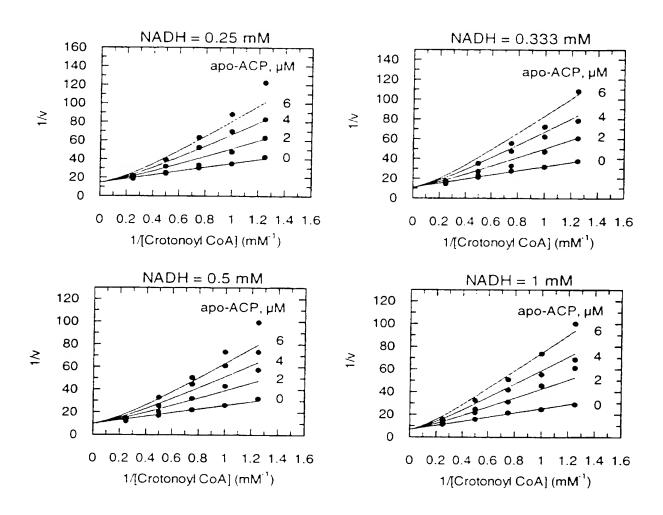
E 
$$\longleftrightarrow$$
 EA  $\longleftrightarrow$  EAB  $\longleftrightarrow$  EPQ

$$V = \frac{V_m[A][B]}{(K_{ta}K_b + K_a[B])\left(1 + \frac{[I]}{K_t}\right) + K_b[A] + [A][B]}$$

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Figure 12. Inhibition by apo-ACP vs. NADH 0.8 mM CCA 1.0 mM CCA iapo-ACPj (μM) [apo-ACP] (µM) 1 / v (min/OD) 1 / v (min/OD) 1/[NADH] (mM<sup>-1</sup>) 1/[NADH] (mM<sup>-1</sup>) 1.33 mM CCA 2.0 mM CCA [apo-ACP] (µM) [apo-ACP] (µM) 1 / v (min/OD) 1 / v (min/OD) 1/[NADH] (mM<sup>-1</sup>) 1/[NADH] (mM<sup>-1</sup>) 4.0 mM CCA Relationship between Ki<sub>(app)</sub> and [CCA] [apo-ACP] (µM) 1 / v (min/OD) Кі(арр) (µМ)  $[CCA]^2 (mM^2)$ 1/[NADH] (mM<sup>-1</sup>)

Figure 13. Inhibition by apo-ACP vs. CCA



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Figure 14. Minimal Kinetic Mechinism for Inhibition by apo-ACP

$$\begin{array}{cccc}
E & \longrightarrow EA & \longrightarrow EAB & \longrightarrow EPQ \\
Kia & & & & & & & & & \\
I & & & & & & & & & \\
& & & & & & & & & \\
EAI & & & & & & & & \\
\end{array}$$

$$v = \frac{V_m[A][B]}{K_{ia}K_b + K_b[A]\left(1 + \frac{[I]}{K_i}\right) + K_a[B] + [A][B]}$$

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Figure 15. Induced Cooperative Inhibition by apo-ACP

- Apo-ACP is uncompetitive versus NADH (Ki(app) and is proportional to the square of [CCA]).
- Apo-ACP is competitive versus crotonoyl CoA and induces negative cooperativity with respect to Cca binding.

$$v = \frac{V_m \left[ \frac{[S]}{K_S} + \frac{[S]^2}{K_S^2} + \frac{[S][I]}{\alpha K_S K_I} \right]}{\left[ 1 + \frac{2[S]}{K_S} + \frac{[S]^2}{K_S^2} + \frac{2[I]}{K_I} + \frac{[I]^2}{K_I^2} + \frac{2[S][I]}{\alpha K_S K_I} \right]}$$

$$Ki = 3 \mu M$$
  
 $\alpha = 15$ 

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## FIGURE 16

(SEQ	ID NO:2;				
-	MUNLENKTY	IMGIANKRSI	AFGVAKVLDÇ	LGAKLWFTYR	KERSRKELEK
51	LLEQLNOPEA	HLYQIDVQSD	EEVINGFEQI	GKDVGNIDGV	YHSIAFANME
101	DLRGRFSETS	REGFLLAQDI	SSYSLTIVAH	EAKKLMPEGG	SIVATTYLGG
151	EFAVQNYNVM	GVAKASLEAN	VHYLALDLGP	DNIRVNAISA	GPIRTLSAKG
201	VGGFNTILKE	IEERAPLKRN	VDQVEVGKTA	AYLLSDLSSG	VTGENIHVDS
251	GFHAIK				

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## FIGURE 17

[SEQ ID NO:1]

-	ATGTTAAAT	C TTGAAAACA	A AACATATGT	C ATCATGGGA	A TOGOTAATAA
51	GCGTAGTATT	GCTTTTGGTG	TCGCTAAAGT	TTTAGATCAA	TTAGGTGCTA
101	AATTAGTATT	TACTTACCGT	AAAGAACGTA	GCCGTAAAGA	GCTTGAAAAA
151	TTATTAGAAC	AATTAAATCA	ACCAGAAGCG	CACTTATATC	AAATTGATGT
201	TCAAAGCGAT	GAAGAGGTTA	TTAATGGTTT	TGAGCAAATT	GGTAAAGATG
251	TTGGCAATAT	TGATGGTGTA	TATCATTCAA	TCGCATTTGC	TAATATGGAA
301	GACTTACGCG	GACGCTTTTC	TGAAACTTCA	CGTGAAGGCT	TCTTGTTAGC
351	TCAAGACATT	AGTTCTTACT	CATTAACAAT	TGTGGCTCAT	GAAGCTAAAA
401	AATTAATGCC	AGAAGGTGGT	AGCATTGTTG	CAACAACATA	TTTAGGTGGC
451	GAATTCGCAG	TTCAAAATTA	TAATGTGATG	GGTGTTGCTA	AAGCGAGCTT
501	AGAAGCAAAT	GTTAAATATT	TAGCATTAGA	CTTAGGTCCT	GATAATATTC
551	GCGTTAATGC	AATTTCAGCT	GGTCCAATCC	GTACATTAAG	TGCAAAAGGT
601	GTGGGTGGTT	TCAATACAAT	TCTTAAAGAA	ATCGAAGAGC	GTGCACCTTT
651	AAAACGTAAC	GTTGATCAAG	TAGAAGTAGG	TAAAACAGCG	GCTTACTTRT
701	TAAGTGACTT	ATCAAGTGGC	GTTACAGGTG	AAAATATTCA	TGTAGATAGC
751	GGATTCCACG	CAATTAAATA	A		